



Amdt C/ #12
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Docket No.: PC-0032 US

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By: [Signature] Printed: Margaret M. Hasson

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Reddy et al.

Title: ASIP-RELATED PROTEINS

Serial No.: 09/757,781

Filing Date: January 09, 2001

Examiner: Rawlings, S.

Group Art Unit: 1642

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Washington, D.C. 20231

RESPONSE TO OFFICE ACTION

Sir:

This paper is responsive to the Office Action dated December 3, 2002. Applicant(s) request reconsideration of the above-referenced patent application in view of the following amendments and remarks.

IN THE SPECIFICATION

✓
Please replace the paragraph beginning at page 31, line 4, with the following rewritten paragraph:

C1
The BLAST software suite, freely available sequence comparison algorithms (NCBI, Bethesda MD), includes various sequence analysis programs including "blastn" that is used to align nucleic acid molecules and BLAST 2 that is used for direct pairwise comparison of either nucleic or amino acid molecules. BLAST programs are commonly used with gap and other parameters set to default settings, e.g.: Matrix: BLOSUM62; Reward for match: 1; Penalty for mismatch: -2; Open Gap: 5 and Extension Gap: 2 penalties; Gap x drop-off: 50; Expect: 10; Word Size: 11; and Filter: on. Identity is measured over the entire length of a sequence or some smaller portion thereof. Brenner et al. (1998; Proc Natl Acad Sci 95:6073-6078, incorporated herein by reference) analyzed the BLAST for its ability to identify structural